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Gencore version 5.1.6  
Run on: September 28, 2004, 09:00:23 (without alignments)

OM protein - protein search, using sw model  
Run on: September 28, 2004, 09:00:23 (without alignments)  
57.362 Million cell updates/sec  
Title: US-10-084-813-13  
Perfect score: 96  
Sequence: 1 SOYQWMKQFQTLKIVLG 18  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 389414 seqs, 51655971 residues

Total number of hits satisfying chosen parameters: 389414  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Issued\_Patents\_Nr:  
1: /cgn2\_6/prodata/2/iaa/5A\_Comb.pep: \*  
2: /cgn2\_6/prodata/2/iaa/6B\_Comb.pep: \*  
3: /cgn2\_6/prodata/2/iaa/6B\_Comb.pep: \*  
4: /cgn2\_6/prodata/2/iaa/PCUTS\_Comb.pep: \*  
5: /cgn2\_6/prodata/2/iaa/backfile11.pep: \*  
6: /cgn2\_6/prodata/2/iaa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	54	4 US-08-833-752-11	Sequence 11, Appl
2	96	100.0	352	3 US-08-66-43D2	Sequence 2, Appl
3	96	100.0	352	3 US-09-087-332A-13	Sequence 13, Appl
4	96	100.0	352	3 US-08-61-105-14	Sequence 14, Appl
5	96	100.0	352	3 US-08-575-967A-2	Sequence 2, Appl
6	96	100.0	352	3 US-09-045-58352	Sequence 32, Appl
7	96	100.0	352	4 US-09-334-785-52	Sequence 5, Appl
8	96	100.0	352	4 US-09-333-752-5	Sequence 52, Appl
9	95	100.0	352	4 US-09-502-783A-2	Sequence 5, Appl
10	96	100.0	352	4 US-09-96-2021	Sequence 2, Appl
11	96	100.0	352	4 US-09-967-468-11	Sequence 1, Appl
12	82	85.4	21	3 US-08-907-468-11	Sequence 11, Appl
13	74	77.1	354	4 US-08-724-984A-2	Sequence 2, Appl
14	47	49.0	354	4 US-08-686-319A-13	Sequence 13, Appl
15	45	46.9	355	3 US-09-045-983-53	Sequence 53, Appl
16	45	46.9	355	4 US-09-034-85-53	Sequence 13, Appl
17	43.5	45.3	352	4 US-09-089-039A-1300	Sequence 1300, A
18	43	44.8	172	4 US-09-021-976-4131	Sequence 4131, A
19	43	44.8	344	3 US-08-681-192-2	Sequence 2, Appl
20	42	43.8	460	3 US-08-935-63-4	Sequence 4, Appl
21	42	43.8	460	4 US-09-594-185-4	Sequence 4, Appl
22	42	43.8	460	4 US-09-0236-3023	Sequence 3023, A
23	41	42.7	160	4 US-09-328-352-6593	Sequence 6593, A
24	41	42.7	160	4 US-09-091-577-2	Sequence 2, Appl
25	41	42.7	363	4 US-09-352-991A-25052	Sequence 25052, A
26	40	41.7	254	4 US-09-134-001C-4582	Sequence 4582, A
27	40	41.7	311	4 US-09-134-001C-5171	Sequence 5171, A

RESULT 1  
US-08-833-752-11  
Sequence 11, Application US/08833752  
GENERAL INFORMATION:  
PATENT NO. 6448375  
APPLICANT: SAMSON, MICHEL  
PARENT: PARMENTIER, MARC  
APPLICANT: VASART, GILBERT  
APPLICANT: VASART, FREDRICK  
TIME OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
TITLE OF INVENTION: ACTIVE AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADRESSEUR: Kroobe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U. S. A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 526  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel R  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
REFERENCE FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 54 amino acids  
TYPE: amino acid  
STRANDEDNESS: Single  
TOPOLOGY: linear  
US-08-833-752-11

Query Match 100.0%; Score 96, DB 4; Length 54:  
Best Local Similarity 100.0%; Pred. No. 5e-09;  
Matches 18; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 4, Appl  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 9, Appl  
Sequence 10, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
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Sequence 62, Appl  
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Sequence 65, Appl  
Sequence 66, Appl  
Sequence 67, Appl  
Sequence 68, Appl  
Sequence 69, Appl  
Sequence 70, Appl

## ALIGNMENTS

Query Match 100.0%; Score 96, DB 4; Length 54:  
Best Local Similarity 100.0%; Pred. No. 5e-09;  
Matches 18; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 4, Appl  
Sequence 5, Appl  
Sequence 6, Appl  
Sequence 7, Appl  
Sequence 8, Appl  
Sequence 9, Appl  
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Sequence 63, Appl  
Sequence 64, Appl  
Sequence 65, Appl  
Sequence 66, Appl  
Sequence 67, Appl  
Sequence 68, Appl  
Sequence 69, Appl  
Sequence 70, Appl

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## On protein - protein search, using SW model

Run on:

September 28, 2004, 08:51:21, Search time 52.525 seconds

(without alignments)

118.345 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QMDFGWMCQLTQVYPIGFFS 22

Scoring table: BLOSUM62

Gapop 10.0, Gapext: 0.5

Searched: 1586107 seqs., 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : ^\_Geneseq\_29Jan04;\*

1: geneseq1980s;\*

2: geneseq2000s;\*

3: geneseq2001s;\*

4: geneseq2002s;\*

5: geneseq2003as;\*

6: geneseq2003bs;\*

7: geneseq2004as;\*

8: geneseq2004bs;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	126	100.0	22	4	ABBB8994	Hab88994 HIV gp120
2	126	100.0	184	2	AAW22406	AAw27406 Inactive
3	126	100.0	215	2	AAW74108	AAw74108
4	126	100.0	215	2	AAW8238	AAw8238 HIV-1 co- acdc102 Human NOV
5	126	100.0	268	7	ACDC1042	ACDC1042 Human NOV
6	126	100.0	268	7	ACDC1044	ACDC1044 Human NOV
7	126	100.0	332	2	AAW26766	AAw6766 Human CCR
8	126	100.0	352	2	AAW24107	AAw24107 Human CCR
9	126	100.0	352	2	AAW27123	AAw27123 Human che- mokine receptor CCR5
10	126	100.0	352	2	AAW27125	AAw27125 Macaque C- hemo-kinin receptor
11	126	100.0	352	2	AAW07602	AAw07602 Human G-P
12	126	100.0	352	2	AAW23835	AAw23835 Human CC
13	126	100.0	352	2	AAW88232	AAw88232 HIV-1 co- receptor CCR5
14	126	100.0	352	3	AAV08128	AAv08128 Human G-P
15	126	100.0	352	4	AAV07089	AAv07089 Human acyl- amino acid transporter
16	126	100.0	352	4	AAE07046	AAe07046 Human G-P
17	126	100.0	352	4	AAE07048	AAe07048 Human G-P
18	126	100.0	352	4	AAE07011	AAe07011 Human CCR
19	126	100.0	352	4	AAE07031	AAe07031 Human che- mokine receptor CCR5
20	126	100.0	352	4	AAE07037	AAe07037 Human G-P
21	126	100.0	352	4	AAE07039	AAe07039 Human G-P
22	126	100.0	352	4	AAE46858	AAe46858 Human HDG
23	126	100.0	352	4	AAE6342	AAe6342 Human Non-endog-
24	126	100.0	352	4	AAE82354	AAe82354 Human CCR
25	126	100.0	352	4	AAE82948	AAe82948 Human HIV

## ALIGNMENTS

RESULT	1
ID	ABBB8994
ABBB8994	standard; peptide: 22 AA.
XX	
AC	ABBB8994;
XX	
DT	23-MAY-2001 (First entry)
XX	
DB	HIV gp120 protein binding peptide #87
XX	
KW	Human chemokine receptor; CD4; HIV; Glycoprotein 120; gp120; antagonist; replication; CCR5; CXCR4; CD4; STRU3; HIV; sapiens.
OS	
XX	
PN	W0200116182-A2.
XX	
PD	08-MAR-2001.
XX	
PP	25-AUG-2000; 2000W0-08023505.
XX	
PR	27-AUG-1999; 99W0-015127P.
XX	
PA	(ISSH ) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Saxinger C;
XX	
WTI	2001-244398/25.
XX	
PS	Claim 21, Page 38, 114pp; English.
XX	
CC	The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRU3, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention.
CC	
CC	Sequence 22 AA;
SQ	Query Match 100.0%; Score 126; DB 4; Length 22; Best Local Similarity 100.0%; Pred. No. 1.2E-12; Best Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 QMDFGWMCQLTQVYPIGFFS 22

|||QWDGFNTMCQTLGIGYPPFS 22

RESIDUE 2  
AAW27405  
ID AAW27406 standard; protein; 184 AA.  
AC  
XX  
AC AAW27406;  
DT 14-APR-1998 (first entry)  
XX  
DB Inactive human CCR5.  
XX  
KW Inactive; human Cys-Cys chemokine receptor-5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; predisposition; resistance; diagnosis; treatment; prevention; inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma; idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer; atherosclerosis; autoimmune disorder.  
XX  
KW Homo sapiens.  
XX  
OS Homo sapiens.  
XX  
PN WO9732019-A2.  
XX  
PR 04-SEP-1997.  
XX  
PP 28-SEP-1997; 97WO-BE0000023.  
XX  
PR 01-MAR-1996; 96EP-00870021.  
PR 06-AUG-1996; 96EP-00870101.  
XX  
PA (EURO-) EUROSCREEN SA.  
XX  
PT Samson M, Parmentier M, Vassart G, Libert P;  
XX  
PA DR WPI/1997-479829/44.  
XX  
PP N-PSDB; AAT90118.  
XX  
PR Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.  
XX  
PA (EURO-) EUROSCREEN SA.  
XX  
PT Samson M, Parmentier M, Vassart G, Libert P;  
XX  
PR WPI/1997-479829/44.  
XX  
DR N-PSDB; AAT90116.  
XX  
PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.  
XX  
PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2  
XX  
PT Claim 7, Fig 1d-e; 94pp; English.  
XX  
PR The present sequence is an inactive human CC (Cys-Cys) chemokine receptor 5 (CCRS), which lacks the last 3 transmembrane regions and the regions involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune disorders. Subjects that express the inactive receptor have a predisposition, or resistance to HIV-1 and/or HIV-2  
XX  
SQ Sequence 215 AA;  
Query Match 100.0%; Score 126; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.2e-11; Mismatches 0; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 QWDGFNTMCQTLGIGYPPFS 22  
DB 93 QWDGFNTMCQTLGIGYPPFS 114  
RESIDUE 4  
AAW88238  
ID AAW88238 standard; protein; 215 AA.  
XX  
AC AAW88238;  
XX  
DT 15-MAR-1999 (first entry)  
XX  
DR HIV-1 co-receptor CCR5 variant CCR5-delta32.  
XX  
KW HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS; gene therapy; human.  
XX  
OS Homo sapiens.  
XX  
PR Key Domain  
PT Location/Qualifiers  
OY 32. .56  
Note: "transmembrane domain 1"

RESULT 3  
AAW27408  
ID AAW27408 standard; protein; 215 AA.  
XX  
AC AAW27408;  
XX  
DT 14-APR-1998. (first entry)

US-09-087-232A-17

Sequence 17, Application US/09087232A

Patent No. 6133431

GENERAL INFORMATION:

APPLICANT: Quillent et al.

TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR

TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSE: Baker &amp; Botts, L.L.P. attn. Lisa Kole

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833.752

FILING DATE: 9-APR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34.115

REFERENCE/DOCKET NUMBER:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-752-6

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833.752

FILING DATE: 9-APR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34.115

REFERENCE/DOCKET NUMBER:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-752-6

Query Match 100.0%; Score 126; DB 3; Length 215;

Best Local Similarity

100.0%; Pred. No. 1.5e-11;

Matches 22; Indels 0; Gaps 0;

Filing Date: 06-JUN-1995

Classification: 435

Attorney/Agent Information:

Name: Steffe, Eric K

Registration Number: 36.688

Reference/Docket Number: 1488.1150000/SKS/KLM

Telecommunication Information:

Telephone: (202) 371-2800

Telex/Fax: (202) 371-5540

Information for Seq ID No: 2:

Sequence Characteristics:

Length: 352 amino acids

Type: amino acid

Topology: linear

Molecule Type: protein

US-08-466-343D-2

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466-343D

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K

REGISTRATION NUMBER: 36.688

REFERENCE/DOCKET NUMBER: 1488.1150000/SKS/KLM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2800

TELEX/FAX: (202) 371-5540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-466-343D-2

Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity

100.0%; Pred. No. 2.5e-11;

Matches 22; Indels 0; Gaps 0;

Filing Date: 06-JUN-1995

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Attorney/Agent Information:

Name: Steffe, Eric K

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Length: 352 amino acids

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US-08-466-343D-2

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466-343D

FILING DATE: 06-JUN-1995

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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

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SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-466-343D-2

Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity

100.0%; Pred. No. 2.5e-11;

Matches 22; Indels 0; Gaps 0;

Filing Date: 06-JUN-1995

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Length: 352 amino acids

Type: amino acid

Topology: linear

Molecule Type: protein

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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466-343D

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

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REGISTRATION NUMBER: 36.688

REFERENCE/DOCKET NUMBER: 1488.1150000/SKS/KLM

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TOPOLOGY: linear

MOLECULE TYPE: protein

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Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity

100.0%; Pred. No. 2.5e-11;

Matches 22; Indels 0; Gaps 0;

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Molecule Type: protein

US-08-466-343D-2

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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

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FILING DATE: 06-JUN-1995

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TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2800

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INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-466-343D-2

Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity

100.0%; Pred. No. 2.5e-11;

Matches 22; Indels 0; Gaps 0;

Filing Date: 06-JUN-1995

Classification: 435

Attorney/Agent Information:

Name: Steffe, Eric K

Registration Number: 36.688

Reference/Docket Number: 1488.1150000/SKS/KLM

Telecommunication Information:

Telephone: (202) 371-2800

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Information for Seq ID No: 2:

Sequence Characteristics:

Length: 352 amino acids

Type: amino acid

Topology: linear

Molecule Type: protein

US-08-466-343D-2

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466-343D

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K

REGISTRATION NUMBER: 36.688

REFERENCE/DOCKET NUMBER: 1488.1150000/SKS/KLM

TELECOMMUNICATION INFORMATION:

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TE

GenCore version 5.1.6  
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On protein - protein search, using sw model

Run on:

September 28, 2004, 09:00:23 / Search time 19.8 Seconds  
 (without alignments)

57.1362 Million call updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 OMDFGNYMCQOLIGLYPGFFS 22

Scoring table: BL05M62

Gapext 10.0, Gapext 0.5

Searched:

389414 seqs, 51625571 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : Issued Patents AA,\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*

2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*

3: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*

4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*

5: /cgn2\_6/ptodata/2/1aa/5C.TUS.COMB.pep:\*

6: /cgn2\_6/ptodata/2/1aa/5D.TUS.COMB.pep:\*

Pred. No. 19 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	126	100.0	184	4	US-08-833-752-4	Sequence 4, Appl
2	126	100.0	215	3	US-09-087-232A-17	Sequence 17, Appl
3	126	100.0	215	4	US-09-087-752-6	Sequence 6, Appl
4	126	100.0	352	3	US-08-465-333D-2	Sequence 2, Appl
5	126	100.0	352	3	US-08-087-232A-13	Sequence 13, Appl
6	126	100.0	352	3	US-08-161-105-14	Sequence 14, Appl
7	126	100.0	352	3	US-08-573-967A-2	Sequence 2, Appl
8	126	100.0	352	3	US-09-045-583-52	Sequence 5, Appl
9	126	100.0	352	4	US-09-517-605-55	Sequence 52, Appl
10	126	100.0	352	4	US-09-534-185-52	Sequence 5, Appl
11	126	100.0	352	4	US-08-833-752-5	Sequence 2, Appl
12	126	100.0	352	4	US-09-502-782A-2	Sequence 1, Appl
13	126	100.0	352	4	US-09-796-202-1	Sequence 9, Appl
14	87	69.0	344	3	US-09-465-333D-9	Sequence 3, Appl
15	87	69.0	347	4	US-08-463-244-3	Sequence 4, Appl
16	87	69.0	360	1	US-08-450-359A-4	Sequence 4, Appl
17	87	69.0	360	3	US-08-045-583-50	Sequence 50, Appl
18	87	69.0	360	4	US-09-053-105-50	Sequence 7, Appl
19	87	69.0	360	4	US-09-053-105-50	Sequence 20, Appl
20	87	69.0	360	4	US-09-131-827A-2	Sequence 4, Appl
21	87	69.0	360	4	US-09-131-827A-2	Sequence 2, Appl
22	87	69.0	360	4	US-09-131-827A-20	Sequence 2, Appl
23	87	69.0	360	5	PCT-NS95-0076-4	Sequence 2, Appl
24	87	69.0	374	1	US-08-450-359A-2	Sequence 2, Appl
25	87	69.0	374	3	US-08-446-659-2	Sequence 2, Appl
26	87	69.0	374	5	PCT-NS95-0076-2	Sequence 2, Appl
27	87	69.0	374	5	US-08-307-499-30	Sequence 30, Appl

#### ALIGNMENTS

RESULT 1	US-08-833-752-4	Sequence 1, Application US/08833752
		Patent No. 6448755
		GENERAL INFORMATION:
		APPLICANT: SAMSON, MICHEL
		APPLICANT: PARMENTIER, MARC
		APPLICANT: WASSET, GILBERT
		APPLICANT: LIBERT, FREDERICK
		TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHERKOVINES RECEPTOR
		NUMBER OF SEQUENCES: 17
		CORRESPONDENCE ADDRESS:
		ADDRESSER: Robbie, Martens, Olson & Bear
		STREET: 610 Newport Center Drive 16th floor
		CITY: Newport Beach
		STATE: CA
		COUNTRY: U.S.A.
		ZIP: 92660
		COMPUTER READABLE FORM:
		COMPUTER: IBM PC compatible
		OPERATING SYSTEM: PC-DOS/MS-DOS
		SOFTWARE: Patentin Release #1.0, Variation #1.25 (BPO)
		CURRENT APPLICATION DATA:
		APPLICATION NUMBER: US/08/833,752
		FILING DATE: 9-28-1997
		CLASSIFICATION: 536
		ATTORNEY/AGENT INFORMATION:
		NAME: Altman, Daniel B
		REGISTRATION NUMBER: 34,115
		REFERENCE/DOCKET NUMBER:
		INFORMATION FOR SEQ ID NO: 4:
		SEQUENCE CHARACTERISTICS:
		LENGTH: 184 amino acids
		TYPE: amino acid
		TOPOLOGY: linear
		MOLCULE TYPE: protein
		US-08-833-752-4
		Query Match
		Best Local Similarity
		100.0%
		Score 126; DB 4; Length 184;
		Matches 22; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
Qy	1	OMDFGNYMCQOLIGLYPGFFS 22
Dy	93	OMDFGNYMCQOLIGLYPGFFS 114

RESULT 2

